Application No. 09/643755

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

☐ 7. Other: _____

Applicant must provide:

☒ An ~~initial or~~ substitute computer readable form (CRF) copy of the "Sequence Listing"

☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

Please return a copy of this notice with your response.

#8

1638

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/643,755B

DATE: 01/23/2002
TIME: 17:11:35

Input Set : A:\Sequence
Output Set: N:\CRF3\01232002\I643755B.raw

<110> APPLICANT: van Rooijen, Gijs
Keon, Richard Glenn
Boothe, Joseph
Shen, Yin

<120> TITLE OF INVENTION: Commercial Production of Chymosin in Plants

<130> FILE REFERENCE: 9369-153

<140> CURRENT APPLICATION NUMBER: 09/643,755B

<141> CURRENT FILING DATE: 2000-08-23

<160> NUMBER OF SEQ ID NOS: 4

<170> SOFTWARE: PatentIn Ver. 2.0

<210> SEQ ID NO: 1

<211> LENGTH: 1173

<212> TYPE: DNA

<213> ORGANISM: Bovine

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(1173)

<400> SEQUENCE: 1

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Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro
             20                  25                  30

ctc tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt   144
Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu
         35                  40                  45

cta gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac   192
Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr
     50                  55                  60

tcc ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat   240
Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp
 65                  70                  75                  80

agt caa tac ttt ggg aag atc tac ctc gga acc ccg cct caa gag ttc   288
Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe
                 85                  90                  95

acc gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc   336
Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile
            100                 105                 110

tac tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga   384
Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg
        115                 120                 125

aag tcg tcc acc ttc cag aac tta ggc aaa ccc ttg tct ata cac tac   432
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RAW SEQUENCE LISTING DATE: 01/23/2002
PATENT APPLICATION: US/09/643,755B TIME: 17:11:35

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66 ggt aca ggt agc atg caa gga atc tta ggc tat gat acc gtc act gtc   480
67 Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val
68 145                 150                 155                 160
70 tcc aac att gtg gac att caa cag aca gta gga ctt agc acc caa gaa   528
71 Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu
72                 165                 170                 175
74 cca ggt gat gtc ttc acc tat gca gaa ttc gat ggc atc ctt ggt atg   576
75 Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met
76             180                 185                 190
78 gca tac cca tcg ctc gcg tca gag tac tcg ata cct gtg ttt gac aac   624
79 Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn
80         195                 200                 205
82 atg atg aac cga cac cta gta gct caa gac ttg ttc tcg gtt tac atg   672
83 Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met
84     210                 215                 220
86 gac agg aat ggc cag gag agc atg ctc acg ctt gga gct att gat cca   720
87 Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro
88 225                 230                 235                 240
90 tcc tac tac aca gga tct ctt cac tgg gtt cca gtc act gtg cag cag   768
91 Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln
92                 245                 250                 255
94 tac tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtt   816
95 Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val
96             260                 265                 270
98 gca tgt gaa ggt gga tgt caa gct atc ttg gat acc ggt acg tcc aag   864
99 Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys
100         275                 280                 285
102 ctg gtc gga cct agc agc gac att ctc aac att cag caa gct att gga   912
103 Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly
104     290                 295                 300
106 gcc aca cag aac cag tac ggt gag ttt gac ata gat tgc gac aac ctt   960
107 Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu
108 305                 310                 315                 320
110 agc tac atg cct aca gtt gtc ttt gag atc aac ggc aag atg tac cca   1008
111 Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro
112                 325                 330                 335
114 ctg acc ccc tcc gcc tat acc agc cag gat caa ggg ttc tgc acc agt   1056
115 Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser
116             340                 345                 350
118 gga ttc cag agt gag aac cat tcc cag aaa tgg atc ttg gga gat gtg   1104
119 Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val
120         355                 360                 365
122 ttc att cgt gag tac tac agc gtc ttt gac agg gcc aac aac ctc gtt   1152
123 Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val
124     370                 375                 380
126 ggg cta gct aaa gca atc tga                                     1173
127 Gly Leu Ala Lys Ala Ile
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RAW SEQUENCE LISTING DATE: 01/23/2002
PATENT APPLICATION: US/09/643,755B TIME: 17:11:35

Input Set : A:\Sequence
Output Set: N:\CRF3\01232002\I643755B.raw

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132 <211> LENGTH: 390
133 <212> TYPE: PRT
134 <213> ORGANISM: Bovine
136 <400> SEQUENCE: 2
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140 Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro
141              20                  25                  30
143 Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu
144          35                  40                  45
146 Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr
147      50                  55                  60
149 Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp
150  65                  70                  75                  80
152 Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe
153                  85                  90                  95
155 Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile
156             100                 105                 110
158 Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg
159         115                 120                 125
161 Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr
162     130                 135                 140
164 Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val
165 145                 150                 155                 160
167 Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu
168                 165                 170                 175
170 Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met
171             180                 185                 190
173 Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn
174         195                 200                 205
176 Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met
177     210                 215                 220
179 Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro
180 225                 230                 235                 240
182 Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln
183                 245                 250                 255
185 Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val
186             260                 265                 270
188 Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys
189         275                 280                 285
191 Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly
192     290                 295                 300
194 Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu
195 305                 310                 315                 320
197 Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro
198                 325                 330                 335
200 Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser
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RAW SEQUENCE LISTING DATE: 01/23/2002
PATENT APPLICATION: US/09/643,755B TIME: 17:11:35

Input Set : A:\Sequence
Output Set: N:\CRF3\01232002\I643755B.raw

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201             340                 345                 350
203 Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val
204         355                 360                 365
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207     370                 375                 380
209 Gly Leu Ala Lys Ala Ile
210 385                 390
213 <210> SEQ ID NO: 3
214 <211> LENGTH: 3957
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <221> NAME/KEY: CDS
220 <222> LOCATION: (1554)..(2726)
222 <220> FEATURE:
223 <223> OTHER INFORMATION: Description of Artificial Sequence: Phaseolin promoter- pre-
pro-
224       chymosin-phaseolin terminator
226 <400> SEQUENCE: 3
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229 tggtttttta cctctattta aaggggtttt ccacctaaaa attctggtat cattctcact 120
231 ttacttgtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180
233 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240
235 ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300
237 agcgttggta gaaagcataa agatttattc ttattcttct tcatataaat gtttaatata 360
239 caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420
241 ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480
243 aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact 540
245 agccattttt ttctttgaat aaaaaaatcc aattatcatt gtatttttt tatacaatga 600
247 aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcatgttat gcaaaattct 660
249 ataattccca tttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720
251 cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaatactcaa 780
253 tattacttct aaaaaattaa ttagatataa ttaaaatatt actttttaa ttttaagttt 840
255 aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900
257 agtttaaagt aaatataagt aatgtagtag agtgttagag tgttacccta aaccataaac 960
259 tataacattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggt 1020
261 atgtaagtcc gtaactagaa ttacagtggg ttgccatggc actctgtggt cttttggttc 1080
263 atgcatgggt cttgcgcaag aaaaagacaa agaacaaaga aaaaagacaa aacagagaga 1140
265 caaaacgcaa tcacacaacc aactcaaatt agtcactggc tgatcaagat cgccgcgtcc 1200
267 atgtatgtct aaatgccatg caaagcaaca cgtgcttaac atgcacttta aatggctcac 1260
269 ccatctcaac ccacacacaa acacattgcc tttttcttca tcatcaccac aaccacctgt 1320
271 atatattcat tctcttccgc cacctcaatt tcttcacttc aacacacgtc aacctgcata 1380
273 tgcgtgtcat cccatgccca aatctccatg catgttccaa ccaccttctc tcttatataa 1440
275 tacctataaa tacctctaat atcactcact tctttcatca tccatccatc cagagtacta 1500
277 ctactctact actataatac cccaacccaa ctcatattca atactactct act atg    1556
278                                                          Met
279                                                           1
281 aac ttc ctt aag tct ttc cct ttc tac gct ttc ctt tgt ttc ggt caa   1604
282 Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly Gln
283               5                  10                  15
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RAW SEQUENCE LISTING DATE: 01/23/2002
PATENT APPLICATION: US/09/643,755B TIME: 17:11:35

Input Set : A:\Sequence
Output Set: N:\CRF3\01232002\I643755B.raw

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285 tac ttc gtt gct gtt act cac gct gct gag atc acc cgc att cct ctc   1652
286 Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro Leu
287          20                  25                  30
289 tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt cta   1700
290 Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu Leu
291      35                  40                  45
293 gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac tcc   1748
294 Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr Ser
295  50                  55                  60                  65
297 ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat agt   1796
298 Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp Ser
299                  70                  75                  80
301 caa tac ttt ggg aag atc tac ctc gga acc ccg cct caa gag ttc acc   1844
302 Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe Thr
303              85                  90                  95
305 gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc tac   1892
306 Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile Tyr
307          100                 105                 110
309 tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga aag   1940
310 Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg Lys
311      115                 120                 125
313 tcg tcc acc ttc cag aac tta ggc aaa ccc ttg tct ata cac tac ggt   1988
314 Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr Gly
315 130                 135                 140                 145
317 aca ggt agc atg caa gga atc tta ggc tat gat acc gtc act gtc tcc   2036
318 Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val Ser
319                 150                 155                 160
321 aac att gtg gac att caa cag aca gta gga ctt agc acc caa gaa cca   2084
322 Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu Pro
323             165                 170                 175
325 ggt gat gtc ttc acc tat gca gaa ttc gat ggc atc ctt ggt atg gca   2132
326 Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met Ala
327          180                 185                 190
329 tac cca tcg ctc gcg tca gag tac tcg ata cct gtg ttt gac aac atg   2180
330 Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn Met
331      195                 200                 205
333 atg aac cga cac cta gta gct caa gac ttg ttc tcg gtt tac atg gac   2228
334 Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met Asp
335 210                 215                 220                 225
337 agg aat ggc cag gag agc atg ctc acg ctt gga gct att gat cca tcc   2276
338 Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro Ser
339                 230                 235                 240
341 tac tac aca gga tct ctt cac tgg gtt cca gtc act gtg cag cag tac   2324
342 Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln Tyr
343             245                 250                 255
345 tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtt gca   2372
346 Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val Ala
347          260                 265                 270
349 tgt gaa ggt gga tgt caa gct atc ttg gat acc ggt acg tcc aag ctg   2420
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VERIFICATION SUMMARY DATE: 01/23/2002
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